WHAT IS CLAIMED IS:

1. A method for analyzing data, comprising performing an unsupervised analysis of data according to a reordered distance matrix.

2. The method of claim 1, wherein said distance matrix is reordered using a weighting function.

3. The method of claims 1 or 2, suitable for automatically and semi-automatically analyzing data.

4. The method of any of claims 1-3, wherein the data comprises a plurality of objects characterized by continuous variables.

5. The method of any of claims 1-4, further comprising:

visualization of the data according to said analysis.

6. The method of claim 5, further comprising:

detecting at least one characteristic of the data according to said visualization.

7. The method of any of claims 1-6, further comprising:

detecting at least one characteristic of the data according to said analysis.

8. The method of claims 6 or 7, wherein the data is analyzed without reference to a predetermined order and/or wherein the data lacks pre-ordering.

9. The method of any of claims 1-8, comprising the SPIN method.

10. The method of claim 9, wherein the SPIN method comprises the *Side-to-Side (STS)* method, featuring a strictly increasing or decreasing vector for reordering said distance matrix.

11. The method of claim 10, wherein said STS method comprises:

Input: D_{nxn} and a strictly increasing vector X

1. Compute $S = D X$.

2. Sort S in descending order to get $S' = P(S)$, where P is the sorting permutation.

3. If $P(S) != S$, set $D = P D P^T$ and go to *stage 1*.

4. Output D.

12. The method of claim 11, further comprising performing stages 1-3 more than once.

13. The method of claims 11 or 12, further comprising using at least one heuristic to reorder *D*.

14. The method of claim 9, wherein the SPIN method comprises the *Neighborhood* method, featuring a matrix of fixed size.

15. The method of claim 14, wherein said Neighborhood method comprises:

Input : D_{nxn} and W_{nxn}

1. Compute $M = D\,W$

2. Set $P = \arg\min_{Q \in S_n} \mathrm{tr}(QM)$.

3. If tr $(P\,M)$!= tr (M), set $D = P\,D\,PT$ and go to 1.

4. Output *D*.

16. The method of claim 15, further comprising performing stages 1-3 more than once.

17. The method of claims 15 or 16, further comprising using at least one heuristic to reorder *D*.

18. The method of claim 14, wherein the *Neighborhood* method features Gaussian smoothing.

19. The method of any of claims 15-18, wherein stage 2 is performed by solving the Linear Assignment Problem.

20. The method of any of claims 1-19, further comprising:

zooming in on a part of the data by separately examining a sub-matrix of the data according to said analysis.

21. The method of claim 20, further comprising:

separately examining a plurality of sub-matrices of the data according to said analysis; and

comparing results of said separate examinations to determine at least one characteristic of the data.

22. The method of any of claims 1 to 21, wherein the data comprises gene expression data and/or data from a gene microarray, comprising data from a large number of genes analyzed simultaneously.

23. The method of any of claims 1 to 21, wherein the data comprises data from expression of genes in cancerous tissue.

24. The method of any of claims 1 to 21, wherein the data comprises data related to a biological process, optionally including a biological cycle.

25. The method of any of claims 1 to 21 adapted for machine vision.

26. A method for analyzing gene expression data and/or data from a gene microarray, comprising data from a large number of genes analyzed simultaneously, comprising:

filtering the data according to a variance filter to form filtered data;

determining a distance matrix for said filtered data; and

reordering said distance matrix to analyze said filtered data.

27. The method of claim 26, further comprising:

analyzing said reordered distance matrix to determine at least one characteristic of said filtered data.

28. The method of claim 27, wherein said reordering is performed according to an automatic and/or semi-automatic, unsupervised analysis.

29. The method of claim 28, wherein said reordering is performed according to SPIN.

30. The method of any of claims 27-29, wherein the data is analyzed to determine a noise level in the data.

31. The method of claim 30, wherein said noise level is used to alter at least one characteristic of the microarray or of an experimental protocol for data collection.

32. The method of any of claims 27-29, wherein the data is analyzed to determine an inherent property of the data other than a property for which the experiment was designed.

33. The method of any of claims 26-32, wherein the data comprises cancer-related data.

34. The method of any of claims 26-33, adapted for ordering both samples and genes.

35. A method for analyzing data related to a biological process, optionally including a biological cycle, comprising the SPIN method.

36. A method for machine vision, comprising the SPIN method.

37. The method of claim 36, wherein the SPIN method is performed for analyzing a distance matrix for visual data.

38. The method of claim 37, further comprising:

zooming in on a part of the data by separately examining a sub-matrix of the data according to said analysis.

39. The method of claim 38, further comprising:

separately examining a plurality of sub-matrices of the data according to said analysis; and

comparing results of said separate examinations to determine at least one characteristic of the data.

40. A method according to any of claims 1-39, for partitioning the data into a plurality of optionally overlapping subsets.

41. The method of claim 40, further comprising:

using the distance matrices calculated from each subset separately to find novel partitions.

42. The method of any of claims 1-41, further comprising implementing the method and presenting the data with an intuitive easy-to-use GUI.

43. A method for analyzing data from expression of genes in cancerous tissue, comprising the SPIN method.

44. The method of any of claims 1-43, further comprising optionally constraining said reordering according to a dendrogram from any hierarchical clustering method.